

APPROVED BY DRAFTSMAN	O. G. FIG.
	CLASS/SUBCLASS

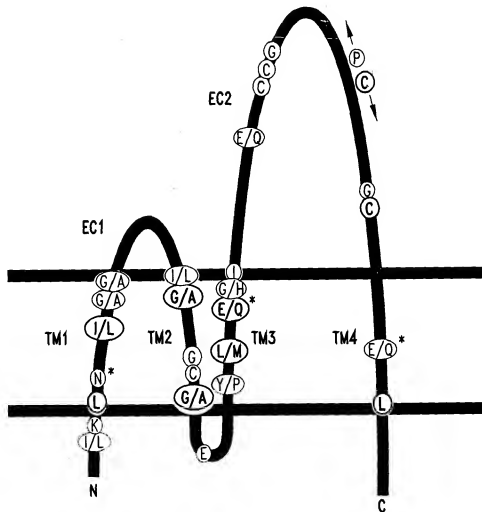
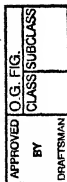


Fig. 1



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1  CTTCCTCGGC CGAGCCGGGC CGCGCGGCCG CTGCCGCCGC CGCGCGCGGA
   GAAGGAGCCG GCTCGGCCCG GCGCGCCGGC GACGCGGGCG GCGCGCGCCT

+1 ]-----
51 TTCTGCTTCT CAGAAGATGC ACTATTATAG ATACTCTAAC GCCAAAGTCA
   AAGACGAAGA GTCTTCTACG TGATAATATC TATGAGATTG CGGTTTCAGT

+1 -----
101 GCTGCTGGTA CAAGTACCTC CTTTTCAGCT ACAACATCAT CTTCTGGTTG
    CGACGACCAT GTTCATGGAG GAAAAGTCGA TGTGTAGTA GAAGACCGAC
    -3 <-----

+3 -----
+1 -----
151 GCTGGAGTTG TCTTCCTTGG AGTCGGGCTG TGGGCATGGA GCGAAAAGGG
    CGACCTCAAC AGAAGGAACC TCAGCCCGAC ACCCGTACCT CGCTTTTCCC
    -3 -----

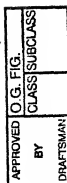
+3 -----
+1 -----
201 TGTGCTGTCC GACCTCACCA AAGTGACCGG GATGCATGGA ATCGACCTTG
    ACACGACAGG CTGGAGTGGT TTA CTG GGC CTACGTACCT TAGCTGGGAC
    -3 -----

+3 -----
+1 -----
251 TGGTGCTGGT CCTGATGGTG GCGTGGTGA TGTTACCCT GGGGTTCCGC
    ACCAGGACCA GGA CTAC CAC CGCACCCT ACAAGTGGGA CCCCAAGCGG
    -3 -----

+3 -----
+1 -----
301 GGCTGCGTGG GGGCTCTGCG GGAGAATATC TGCTTGCTCA ACTTTTCTG
    CCGACGACC CCGAGACGC CCTCTTATAG ACGAACGAGT TGA AAAAGAC
    -3 -----

+3 -----
+1 -----
351 TGGCACCATC GTGCTCATCT TCTTCCTGGA GCTGGCTGTG GCCGTGCTGG
    ACGTGGTAG CACGAGTAGA AGAAGGACCT CGACCGACAC CGGCACGACC

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+3 -----
+1 -----
401 CCTTCCTGTT CCAGGACTGG GTGAGGGACC GGTTCGGGA GTTCTTCGAG
    GGAAGGACAA GGTCTGACC CACTCCCTGG CCAAGGCCCT CAAGAAGCTC
-3 -----

+3 -----
+1 -----

                                ClaI
                                ~~~~~
451 AGCAACATCA AGTCTACCG GGACGATATC GATCTGCAA ACCTCATCGA
    TCGTTGTAGT TCAGGATGGC CCTGCTATAG CTAGACGTTT TGGAGTAGCT
-3 -----[

+3 ----->
+1 -----
501 CTCCTTCAG AAAGCTAACC AGTGTGTGG CGCATATGGC CTAAGAGCT
    GAGGGAAGTC TTTCGATTGG TCACGACACC GCGTATACCG GGACTTCTGA

+1 -----
551 GGGACCTCAA CGTCTACTTC AATTGCAGCG GTGCCAGCTA CAGCCGAGAG
    CCCTGGAGTT GCAGATGAAG TTAACGTCGC CACGGTCGAT GTCGGCTCTC

+1 -----
601 AAGTCCGGGG TCCCCTTCTC CTGCTGCGTG CCAGATCCTG CGCAAAAAGT
    TTCACGCCC AGGGAAGAG GACGACGCAC GGTCTAGGAC GCGTTTTTCA

+1 -----
651 TGGAACACA CAGTGTGGAT ATGATGTCAG GATTGAGCTG AAGAGCAAGT
    ACACTTGTGT GTCACACCTA TACTACAGTC CTAAGTCGAC TTCTCGTTCA

+1 -----
701 GGGATGAGTC CATCTTCACG AAAGGCTGCA TCCAGGCGCT GGAAGCTGG
    CCCTACTCAG GTAGAAGTGC TTTCGACGT AGGTCCGCGA CCTTCGACC

+1 -----
751 CTCCTCGGGA ACATTTACAT TGTGGCTGGC GTCTTCATCG CCATCTCGCT
    GAGGGCGCCT TGAAATGTA ACACCGACCG CAGAAGTAGC GGTAGAGCGA
-1 -----<

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Fig. 2B

Title: TETRASPAN PROTEIN AND USES THEI

Inventors: Christoph Reinhard et al. Serial No. 09/905,674 Docket No. PP-01700.002/200130.521

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+1 -----
801 GTTGCAGATA TTTGGCATCT TCCTGGCAAG GACGCTGATC TCAGACATCG
CAACGTCTAT AAACCGTAGA AGGACCGTTC CTGCGACTAG AGTCTGTAGC
-1 -----

+1 -----
851 AGGCAGTGAA GGCCGGCCAT CACTTCTGAG GAGCAGAGTT GAGGGAGCCG
TCCGTCACTT CCGGCCGGTA GTGAAGACTC CTCGTCTCAA CTCCTCGGC
-1 -----

901 AGCTGAGCCA CGCTGGGAGG CCAGAGCCTT TCTCTGCCAT CAGCCCTACG
TCGACTCGGT GCGACCCTCC GGTCTCGGAA AGAGACGGTA GTCGGGATGC
-1 -----

+1 -----]-----
951 TCCAGAGGGA GAGGAGCCGA CACCCCCAGA GCCAGTGCCC CATCTTAAGC
AGGTCTCCCT CTCCTCGGCT GTGGGGGTCT CGGTACCGG GTAGAATTGC
-1 ----- [

+1 -----
1001 ATCAGCGTGA CGTGACCTCT CTGTTTCTGC TTGCTGGTGC TGAAGACCAA
TAGTCGCACT GCACTGGAGA GACAAAGACG AACGACCACG ACTTCTGGTT

+1 -----
1051 GGGTCCCCCT TGTACCTGC CCAAAGTGT GACTGCATCC CTCTGGAGTC
CCCAGGGGGA ACAATGGACG GGTTTGAACA CTGACGTAGG GAGACCTCAG

+1 -----
1101 TACCCAGAGA CAGAGAATGT GTCTTTATGT GGGAGTGGTG ACTCTGAAGG
ATGGGTCTCT GTCTTTACA CAGAAATACA CCCTCACCAC TGAGACTTTC
-1 <-----

+1 -----
PstI

1151 ACAGAGAGGG CTCCTGTGGC TGCCAGGAGG GCTTGACTCA GACCCCTCGC
TGCTCTCCC GAGGACACCG ACGGTCTCC CGAACTGAGT CTGGGGGAGC
-1 -----

Fig. 2C

APPROVED BY DRAFTSMAN	O. G. FIG.
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+1 -----
Pst1
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1201 AGCTCAAGCA TGTCTGCAGG ACACCCTGGT CCCYTYTCCA YTGGCWTCCA
TCGAGTTCGT ACAGACGTCC TGTGGGACCA GGRARAGGT RACCGWAGT
-1 -----

+1 ----->
1251 GACATCTGCT TTGGGTCATC CACATCTGTG GGTNGGCCGT GGTAGAGGG
CTGTAGACGA AACCCAGTAG GTGTAGACAC CCANCCGGCA CCCATCTCCC
-1 -----

1301 ACCCACAGGC GTGGACAGGG CATCTCTCTC CATCAAGCAA AGCAGCATGG
TGGGTGTCCG CACCTGTCCC GTAGAGAGAG GTAGTTCGTT TCGTCGTACG
-1 -----[

1351 GGGGCCTTGC CGTAAACGGG AGGCGNGACG TTGCCCC
CCCCGGAACG GCATTTGCCC TCCGCNCTGC AACCGGG

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Fig. 2D

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1 MHYYRYRNAK VSCWYKYLFF SYNIIFWLAG VVFLGVGLWA WSEKGVLSDL
 51 TKVTRMHGID PVVLVLMVGVMFTLGFAGC VGALRENICL LNFFCGTIVL
 101 IFFLELAVAV LAFLFQDWVR DRFREFFESN IKSYYRDDIDL QNLIDSLQKA
 151 NQCCGAYGPE DWDLVNYVNC SGASYSREKC GVPFSCCPVD PAQKVVTQC
 201 GYDVRIQLKS KWDESIFTKG CIQALESWLP RNIIYVAGVF IAISLLQIFG
 251 IFLARTLISD IEAVKAGHHF

Fig. 3

NTSP5:P104	CHIR22-1	TGCAGCCTTTGCTGAAGATGGACTC	25 (7-11-7)
NTSP5:P727	CHIR22-2	CCCCATGCTGCTTTGCTTGATGGAG	25 (7-11-7)
NTSP5:P285	CHIR22-3	GCTCAGCTCGGCTCCCTCAACTC	23 (7-9-7)
NTSP5:P456	CHIR22-4	CACAAGTTTGGGCAGGTAACAAGGG	25 (7-11-7)
NTSP5:P395	CHIR22-5	AGAGGTCACGTCACGCTGATGCTTA	25 (7-11-7)
NTSP5:P104	CHIR22-1RC	CTCAGGTAGAAGTGCTTTCCGACGT	25 (7-11-7)
NTSP5:P727	CHIR22-2RC	GAGGTAGTTCGTTTCGTCGTACCCC	25 (7-11-7)
NTSP5:P285	CHIR22-3RC	CTCAACTCCCTCGGCTCGACTCG	23 (7-9-7)
NTSP5:P456	CHIR22-4RC	GGGAACAATGGACGGGTTTGAACAC	25 (7-11-7)
NTSP5:P395	CHIR22-5RC	ATTCGTAGTCGCACTACGCTGGAGA	25 (7-11-7)

Fig. 4

APPROVED	O.G. FIG.
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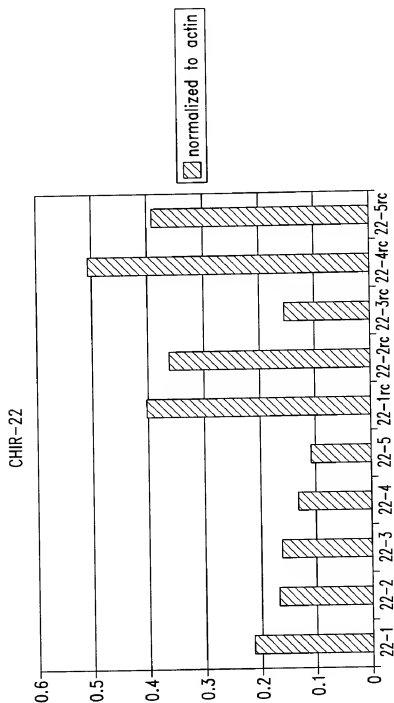


Fig. 5

APPROVED	O.G. FIG.
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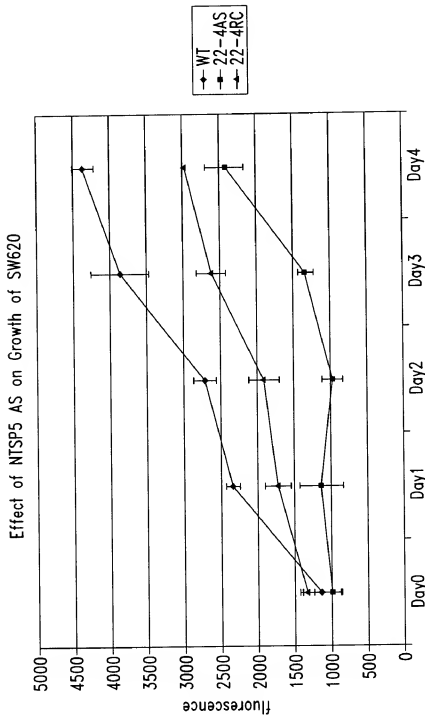


Fig. 6